



5398-027-27CONT.ST25

SEQUENCE LISTING

<110> Cohen, Stanley N.
Li, Limin

<120> Mammalian Tumor Susceptibility Genes and Their Uses

<130> 5398-027-27CONT

<140> US 10/697,720

<141> 2003-10-29

<150> US 09/804,690

<151> 2001-03-12

<150> US 09/146,187

<151> 1998-09-01

<150> US 08/977,818

<151> 1997-11-25

<150> US 08/670,274

<151> 1996-06-13

<150> US 08/585,758

<151> 1996-01-16

<150> US 60/006,856

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<211> 1448

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atg atg tcc aag tac aaa tat aga gat cta acc gtc cgt caa act gtc 108
Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
1 5 10 15

aat gtc atc gct atg tac aaa gat ctc aaa cct gta ttg gat tca tat 156
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

gtt ttt aat gat ggc agt tcc agg gag ctg gtg aac ctc act ggt aca 204
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
35 40 45
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atc cca gtg cgt tat cga ggt aat ata tat aat att cca ata tgc ctg	252
Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu	
50 55 60	
tgg ctg ctg gac aca tac cca tat aac ccc cct atc tgt ttt gtt aag	300
Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys	
65 70 75 80	
cct act agt tca atg act att aaa aca gga aag cat gtg gat gca aat	348
Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn	
85 90 95	
ggg aaa atc tac cta cct tat cta cat gac tgg aaa cat cca cgg tca	396
Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser	
100 105 110	
gag ttg ctg gag ctt att caa atc atg att gtg ata ttt gga gag gag	444
Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu	
115 120 125	
cct cca gtg ttc tcc cgg cct act gtt tct gca tcc tac cca cca tac	492
Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr	
130 135 140	
aca gca aca ggg cca cca aat acc tcc tac atg cca ggc atg cca agt	540
Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser	
145 150 155 160	
gga atc tct gca tat cca tct gga tac cct ccc aac ccc agt ggt tat	588
Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr	
165 170 175	
cct ggc tgt cct tac cca cct gct ggc cca tac cct gcc aca aca agc	636
Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser	
180 185 190	
tca cag tac cct tcc cag cct cct gtg acc act gtt ggt ccc agc aga	684
Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg	
195 200 205	
gat ggc aca atc agt gag gac act atc cgt gca tct ctc atc tca gca	732
Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala	
210 215 220	
gtc agt gac aaa ctg aga tgg cgg atg aag gag gaa atg gat ggt gcc	780
Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala	
225 230 235 240	
cag gca gag ctt aat gcc ttg aaa cga aca gag gaa gat ctg aaa aaa	828
Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys	
245 250 255	
ggc cac cag aaa ctg gaa gag atg gtc acc cgc tta gat caa gaa gta	876
Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val	
260 265 270	
gct gaa gtt gat aaa aac ata gaa ctt ttg aaa aag aag gat gaa gaa	924
Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu	
275 280 285	

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cta agt tct gct ctg gag aaa atg gaa aat caa tct gaa aat aat gat 972
Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
290 295 300

att gat gaa gtt atc att ccc aca gcc cca ctg tat aaa cag att cta 1020
Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
305 310 315 320

aat ctg tat gca gag gaa aat gct att gaa gac act atc ttt tac ctt 1068
Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
325 330 335

gga gaa gct ttg cgg cgg gga gtc ata gac ctg gat gtg ttc ctg aaa 1116
Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
340 345 350

cac gtc cgc ctc ctg tcc cgt aaa cag ttc cag cta agg gca cta atg 1164
His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
355 360 365

caa aag gca agg aag act gcg ggc ctt agt gac ctc tac tgacatgtgc 1213
Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
370 375 380

tgtcagctgg agaccgacct ctccgtaaag cattcttttc ttcttctttt tctcatcagt 1273
agaaccacaca ataagttatt gcagttttatc attcaagtgt taaatatttt gaatcaataa 1333
tatattttct gtttcctttg ggtaaaaact ggcttttatt aatgcacttt ctaccctctg 1393
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20 25 30
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
35 40 45
Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu
50 55 60
Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65 70 75 80
Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
85 90 95
Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
100 105 110
Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
115 120 125
Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
130 135 140
Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
145 150 155 160

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Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
 165 170 175
 Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
 180 185 190
 Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
 195 200 205
 Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
 210 215 220
 Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
 225 230 235 240
 Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
 245 250 255
 Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
 260 265 270
 Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
 275 280 285
 Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
 290 295 300
 Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
 305 310 315 320
 Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
 325 330 335
 Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
 340 345 350
 His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
 355 360 365
 Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
 370 375 380

<210> 3

<211> 1494

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 3

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atggtgtcca agtacaata cagagacctt actgtacgtg aaactgtcaa tggtattact 180
ctatacaaag atctcaaacc tgttttgat tcatatgttt ttaacgatgg cagttccagg 240
gaactaatga acctacttg aacaatccct gtgccttata gaggtaatac atacaatatt 300
ccaatatgcc tatggctact ggacacatac ccatataatc cccctatctg ttttgtaaag 360
cctactagtt caatgactat taaaacagga aagcatgttg atgcaaatgg gaagatatat 420
cttccttata tacatgaatg gaaacaccca cagtcagact tgttggggct tattcaggct 480
atgatttgtg tatttgaga tgaacctcca gtcttctctc gtcctatttc ggcactctat 540
ccgccatacc aggcaacggg gccaccaaact atttcttaca tgccaggcat gccagggtga 600
atctctccat acccatccgg ataccctccc aatcccagtg gttaccagg ctgtccttac 660
ccacctggtg gtccatatcc tgccacaaca agttctcagt acccttctca gcctcctgtg 720
accactgttg gtcccagtag ggatggcaca atcagcgagg acaccatccg agcctctctc 780
atctctgcgg tcagtgaaca actgagatgg cggatgaagg aggaaatgga tcgtgcccag 840
gcagagctca atgccttgaa acgaacagaa gaagacctga aaaagggta ccagaaactg 900
gaagagatgg ttaccggttt agatcaagaa gttagccgagg ttgataaaaa catagaactt 960
ttgaaaaaga aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtctgaa 1020
aacaatgata tcgatgaagt tatcattccc acagctccct tatacaaaca gatcctgaat 1080
ctgtatgcag aagaaaacgc tattgaagac actatctttt acttgggaga agccttgaga 1140
aggggcgtga tagacctgga tgtcttctct aagcatgtac gtcttctgtc ccgtaaacag 1200

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ttccagctga gggcactaat gcaaaaagca agaaagactg ccggtctcag tgacctctac 1260
tgactttctct gataccagct ggaggttgag ctcttcttaa agtattcttc tcttcctttt 1320
atcagtaggt gccagaata agttattgca gtttatcatt caagtgtaaa atattttgaa 1380
tcaataatat attttctgtt ttcttttggg aaagactggc ttttattaat gcactttcta 1440
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<210> 4

<211> 390

<212> PRT

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<220>

<223> primer

<400> 4

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      20      25      30
Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
      35      40      45
Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
      50      55      60
Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
      65      70      75      80
Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
      85      90      95
Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
      100     105     110
Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
      115     120     125
Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
      130     135     140
Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
      145     150     155     160
Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
      165     170     175
Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
      180     185     190
Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
      195     200     205
Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
      210     215     220
Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
      225     230     235     240
Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
      245     250     255
Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
      260     265     270
Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
      275     280     285
Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
      290     295     300
Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
      305     310     315     320
Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
      325     330     335
Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
      340     345     350

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Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg
 355 360 365
 Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
 370 375 380
 Gly Leu Ser Asp Leu Tyr
 385 390

<210> 5
 <211> 27
 <212> RNA
 <213> Artificial Sequence

<220>
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<400> 5
 aggucaugau ugugguauuu ggagaug 27

<210> 6
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<220>
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<400> 6
 caucuccaaa uaccacaauc augaccu 27

<210> 7
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<400> 7
 caucauac augaggtggc ttatgagtat ttcttccag 39

<210> 8
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<220>
 <223> primer

<400> 8
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<210> 9
 <211> 28
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<220>
 <223> primer

<400> 9
 ctgataccag ctggagggttg agctcttc 28
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 <400> 10
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 <223> primer
 <400> 11
 gagaccgacc tctccgtaaa gcattctt 28
 <210> 12
 <211> 28
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 <400> 12
 tagcccagtc agtcccagca cagcacag 28
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 <400> 13
 atttagcagt cccaacattc agcacaaa 28
 <210> 14
 <211> 25
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 <223> primer
 <400> 14
 gtcttctggg tggcagtgat ggcatt 25
 <210> 15

<211> 27
 <212> DNA
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 <220>
 <223> primer

 <400> 15
 cgggtgtcgg agagccagct caagaaa 27

 <210> 16
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 <212> DNA
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 <220>
 <223> primer

 <400> 16
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 <210> 17
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 <220>
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 <400> 17
 cctccagctg gtatcagaga agtcgt 26

 <210> 18
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 <400> 18
 cacagtcaga cttgttgggg cttattc 27

 <210> 19
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 <212> PRT
 <213> Artificial Sequence

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 <223> primer

 <400> 19
 His Thr His Leu Ala Met Asx Asp Ala
 1 5

 <210> 20
 <211> 10
 <212> PRT

<213> Artificial Sequence

<220>

<223> primer

<221> VARIANT

<222> 2

<223> Xaa = Any Amino Acid

<400> 20

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